

Figure 1.

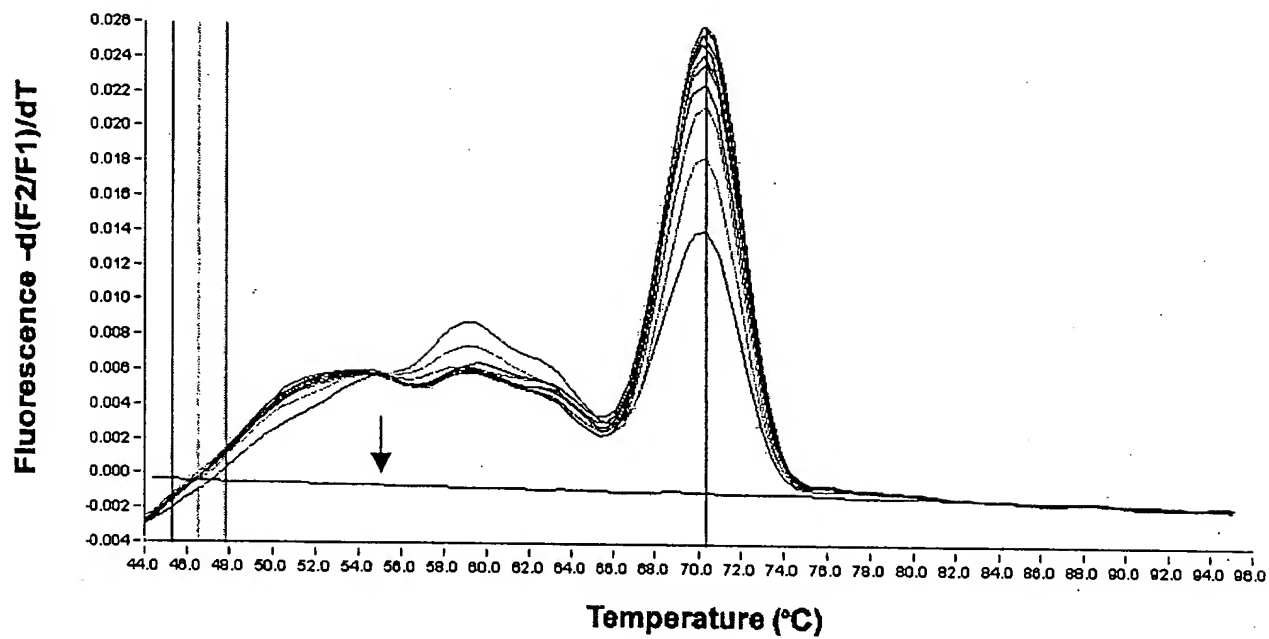


Figure 2.

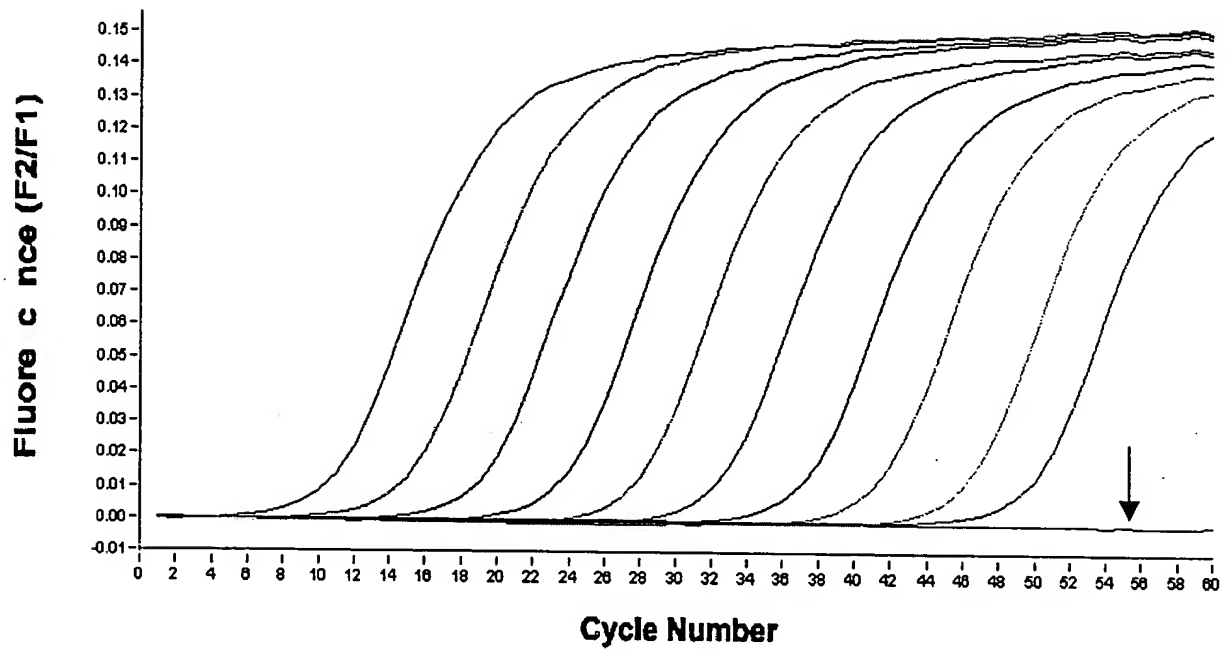


Figure 3.

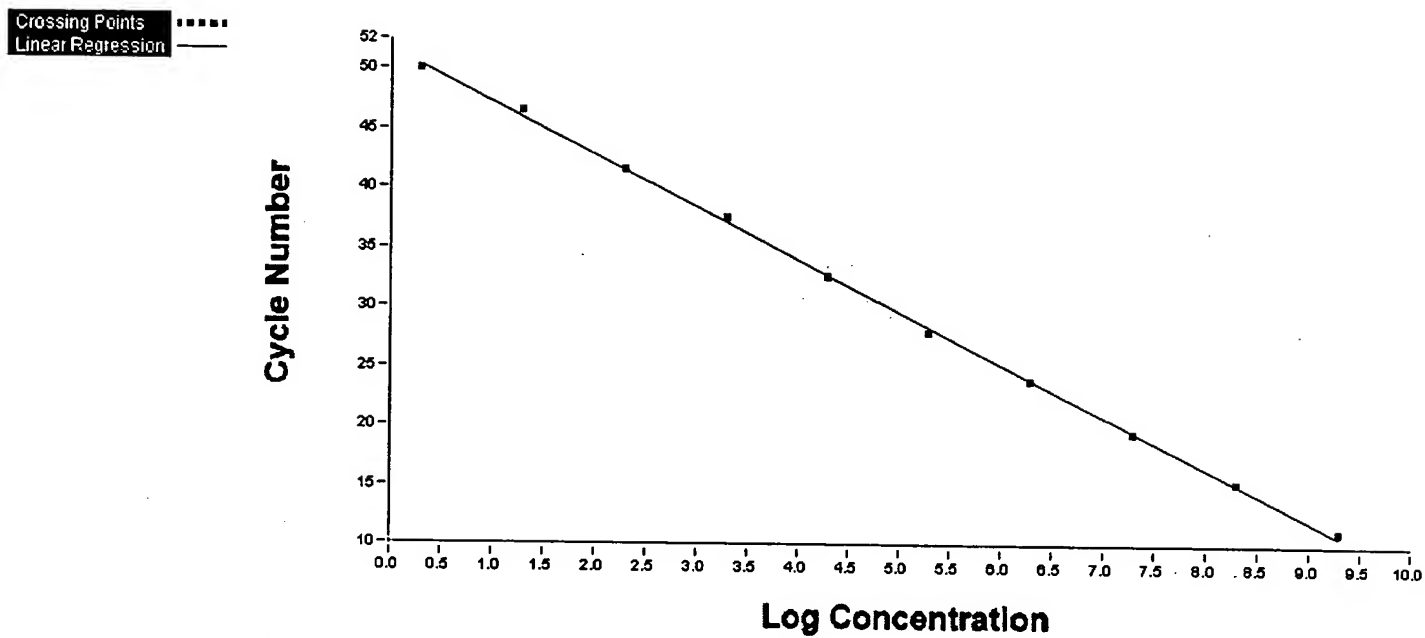


Figure 4.

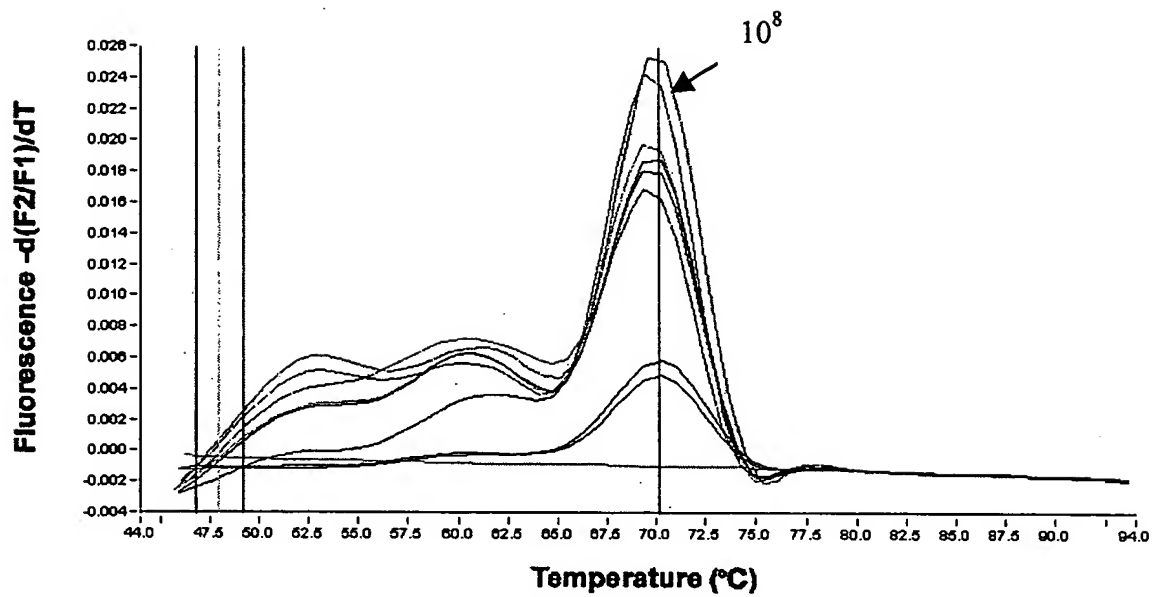


Figure 5

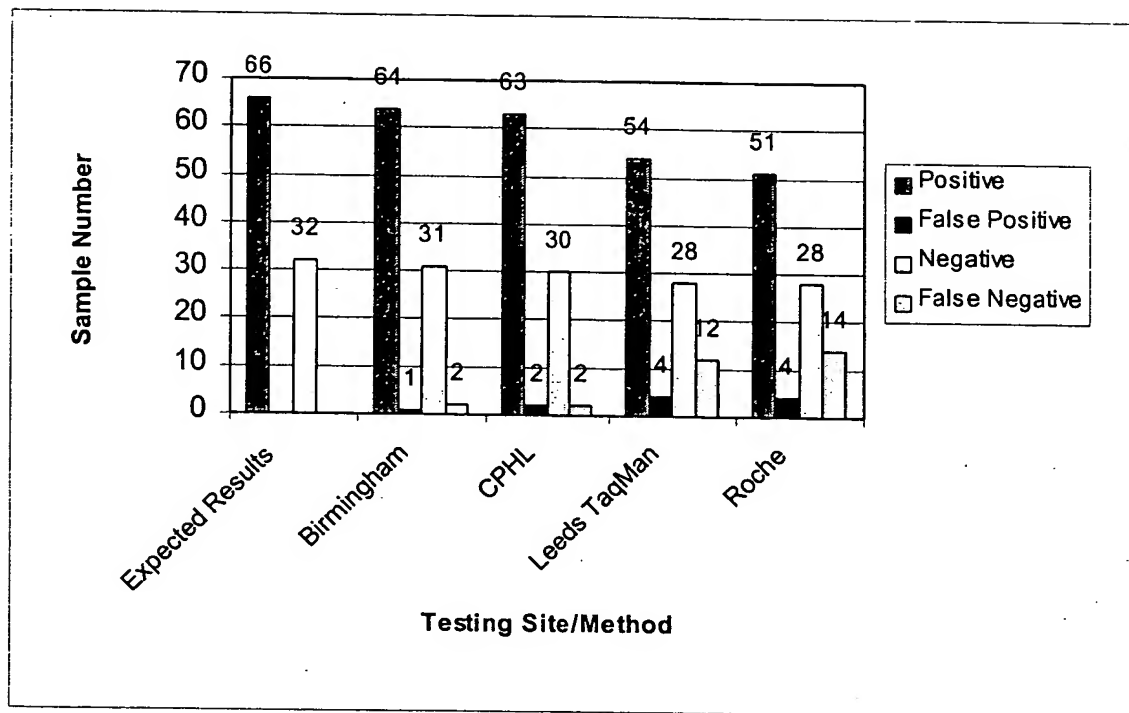


Figure 6

└─>gi|18025465|gb|AY037858.1| **D** Cercopithicine herpesvirus 15 strain LCL8664,  
complete genome  
Length = 171096

Score = 125 bits (63), Expect = 3e-27  
Identities = 84/91 (92%)  
Strand = Plus / Plus

Query: 32 tctggtgtccgggggataatggagtcacatccaggcttgggcacatctgcttcaacag 91  
|||||  
Sbjct: 84022 tctggtgtccgggggataatggagtcacatccaggcttgggcacatctgcttcatcagg 84081

Query: 92 aggcgcagcctgtcattttcagatgatttg 122  
| ||| ||| |||||  
Sbjct: 84082 atgcgtagccgttcattttccgatgatttg 84112

Score = 125 bits (63), Expect = 3e-27  
Identities = 194/237 (81%), Gaps = 3/237 (1%)  
Strand = Plus / Plus

Query: 583 cagtagaattgtctccagggttgaggtgcttctccccggcttggttagtctgttgattct 642  
|||||  
Sbjct: 84718 cagtagaattgtctccagggttgaggtgcttctccccggcttggtgaaactgttgaatct 84777

Query: 643 gggttatgtcggagactgggaacagctgaggtgctgcataagcttgataagcattctcag 702  
|||| | ||| ||| |||||  
Sbjct: 84778 gggtaagctctgggacttgagcagctgaggtgctgcataatgtcggataaagattctcag 84837

Query: 703 gagcaggctgaggggagaaaaccacgacccagtcggagcgggtgaaacatgataggcag 762  
|| || |||| |||| |||||  
Sbjct: 84838 gattagtctgaaaagcaggaaaccactgcccagtaggagcggctgaaaggtgataagcag 84897

Query: 763 t---tagctggccttgtggcagaggctctggcagcaccggccacagcacacaaggca 816  
||| | ||||| |||||  
Sbjct: 84898 tgggctgctgaacatgtggcagtggtccgacagcaccggccaaagcacacaaggca 84954

Score = 113 bits (57), Expect = 1e-23  
Identities = 105/121 (86%)  
Strand = Plus / Plus

Query: 215 acctcacggtagtgtgctgcagcagttgcttaaacttgcccggcattttctggaagccacc 274  
|||||  
Sbjct: 84229 acctcacggtagtgtgctgcagaagattcttgaacctggctcggcattttctggaagccacc 84288

Query: 275 cgattcttgatcgctttattttctagttcagaatcgcatctcctccagctgcgagcaagg 334  
|| ||||| ||||| |||||  
Sbjct: 84289 cggttcttgtaacgctttattttcaagttcagagccacactcgtccagctacaagcaagg 84348

Query: 335 a 335  
|  
Sbjct: 84349 a 84349

Score = 54.0 bits (27), Expect = 8e-06  
Identities = 36/39 (92%)  
Strand = Plus / Plus

Attorney Docket No.: 23660/2  
DETECTION OF EPSTEIN BARR VIRUS  
Applicant(s): Melvyn Smith  
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Query: 824 ttgcgatggccctcccaggtcctgatagactctggtagc 862  
||||||| || ||||||||||||||||| |||||  
Sbjct: 84971 ttgcgatgggtccacccaggtcctgatagactctagtagc 85009

Score = 36.2 bits (18), Expect = 2.0  
Identities = 24/26 (92%)  
Strand = Plus / Plus

Query: 443 taccgattctggctgttggtggtttcc 468  
||||||| ||||| ||| |||||  
Sbjct: 84578 taccgattctggctgttggtggtttcc 84603

Attorney Docket No.: 23660/2  
DETECTION OF EPSTEIN BARR VIRUS  
Applicant(s): Melvyn Smith  
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	1		50
BZLF1	TTAGAAATTT AAGAGATCCT CGTGTA AAC ATCTGGTGT C CGGGGGATAA		
PROBE	.....		
BZLF1F	.....		
BZLF1R	.....		
Consensus	.....		
	51		100
BZLF1	TGGAGTCAAC ATCCAGGCTT GGGCACATCT GCTTCAACAG GAGGCGCAGC		
PROBE	.....		
BZLF1F	.....GCACATCT GCTTCAACAG		
BZLF1R	.....		
Consensus	.....		
	101		150
BZLF1	CTGTCATTTT CAGATGATTT GGCAGCAGCC ACCTGCGGAC AAAAATCAGG		
PROBE	.....		
BZLF1F	.....		
BZLF1R	.....		
Consensus	.....		
	151		200
BZLF1	CGTTTAGATG GGGCATTAT GTTTGGGACG CTAGCCGCCT GGGCATTTCGT		
PROBE	.....GCCGCCT		
BZLF1F	.....		
BZLF1R	.....		
Consensus	.....		
	201		250
BZLF1	GTTAGTATAT ACTGACCTCA CGGTAGTGCT GCAGCAGTTG CTAAACTTG		
PROBE	GTTA.....		
BZLF1F	.....		
BZLF1R	...GTATAT ACTGACCTCA CG.....		
Consensus	...gtatat actgacctca cg.....		
	251		300
BZLF1	GCCCCGCATT TTCTGGAAGC CACCCGATTC TTGTATCGCT TTATTTCTAG		
PROBE	.....		
BZLF1F	.....		
BZLF1R	.....		
Consensus	.....		
	301		350
BZLF1	TTCAGAATCG CATTCTCCA GCTGCGAGCA AGGGAATGCG TTAACAAG		
PROBE	.....		
BZLF1F	.....		
BZLF1R	.....		
Consensus	.....		
	351		400
BZLF1	TGGTGCCTAG TCAGTTGAAA CAAGCCCCAC CATCCGCTGC CGCCCCCTCA		
PROBE	.....		
BZLF1F	.....		
BZLF1R	.....		
Consensus	.....		
	401		450
BZLF1	TGAGCCCCAC CGTCCGCTGC CGCCCCTCCT TGAGCCCCCTC CTTACCGATT		
PROBE	.....		
BZLF1F	.....		
BZLF1R	.....		
Consensus	.....		

Figure 7